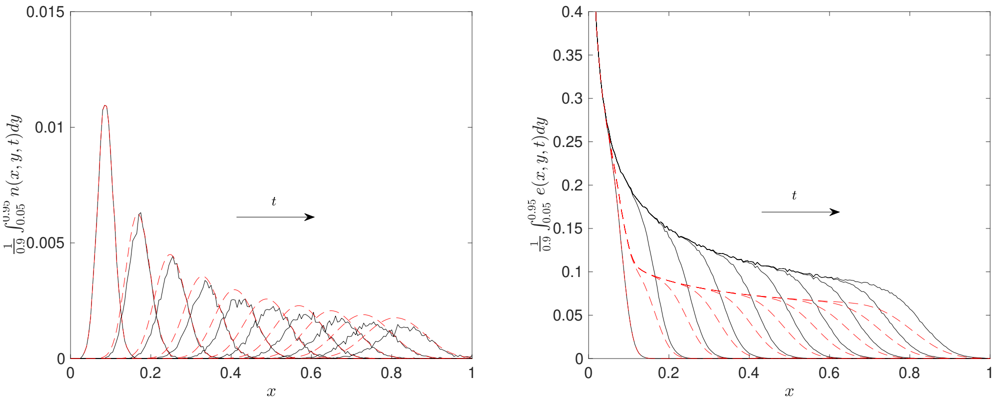
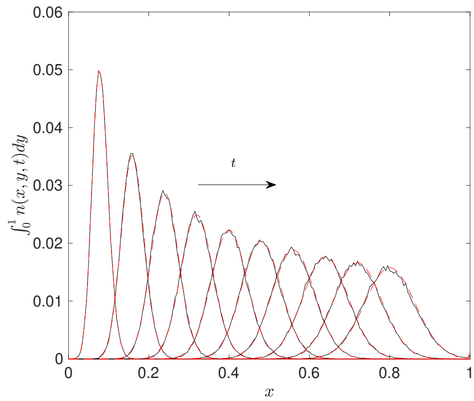


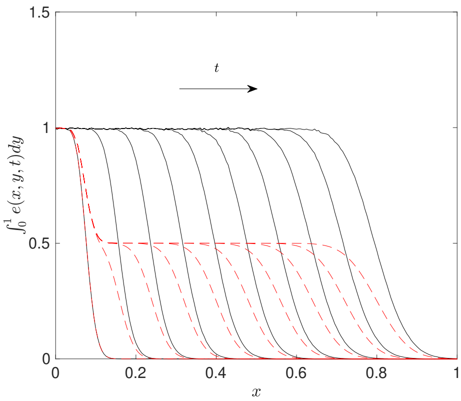
(a) Tip Cells

(b) Stalk Cells

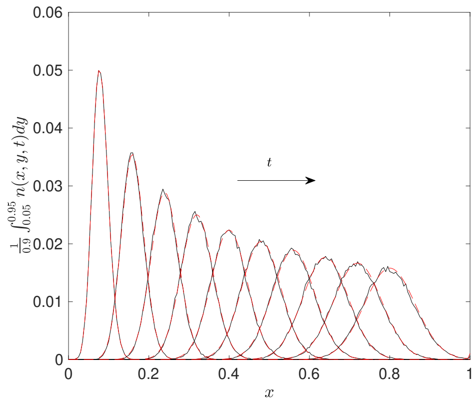
Figure 1: Solutions of the (a) tip cell, $n(x, y, t)$, and (b) stalk cell, $e(x, y, t)$, densities given by the P–ABM and 2D snail-trail model subject to the TAF field $c(x, y) = x$, column averaged in the y-direction, at $t = 0.2$, 0.4, ..., 2, with $\kappa(x, y) = 1$. Column averages were computed over the interval $y \in [0.05, 0.95]$ in order to exclude possible edge effects. Key: P–ABM distribution (solid black lines); column averaged 2D snail-trail solution (red dashed lines). For colors, we refer to the online article. Initial conditions and parameter values: as in Figures 2 and 9 of the main text.



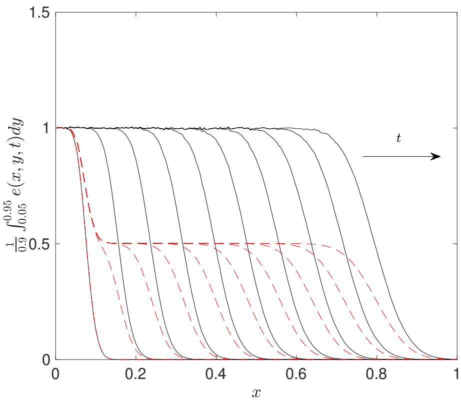
(a) Tip Cells, $y \in (0, 1)$



(b) Stalk Cells, $y \in (0, 1)$

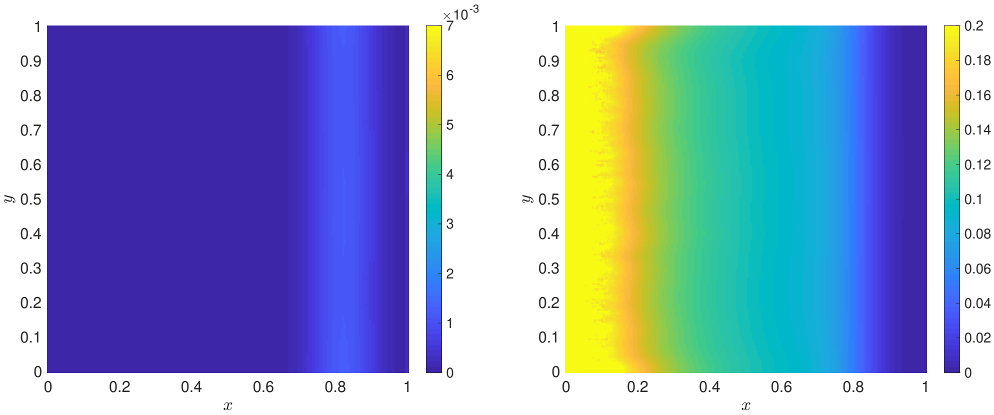


(c) Tip Cells, $y \in (0.05, 0.95)$



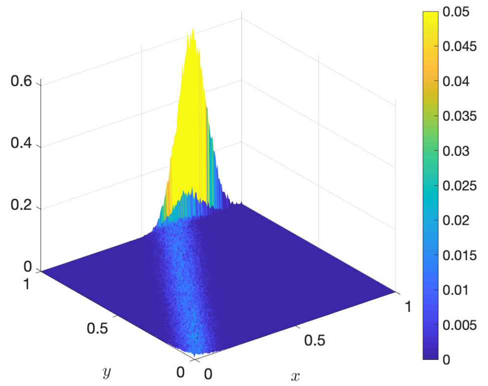
(d) Stalk Cells, $y \in (0.05, 0.95)$

Figure 2: Solutions of the (a, c) tip cell, $n(x, y, t)$, and (b, d) stalk cell, $e(x, y, t)$ densities given by the P–ABM and 2D snail-trail model, column averaged in the y-direction, at $t = 0.2$, 0.4, ..., 2, with $\kappa(x, y) = 1$ and $\lambda = \beta_e = \beta_n = 0$. Column averages were computed over the interval (a, b) $y \in [0, 1]$ and (c, d) $y \in [0.05, 0.95]$ in order to determine if edge effects caused differences between the two sets of results. Key: P–ABM distribution (solid black lines); column averaged 2D snail-trail solution (red dashed lines). The P–ABM was simulated with no anastomosis or branching allowed. The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.

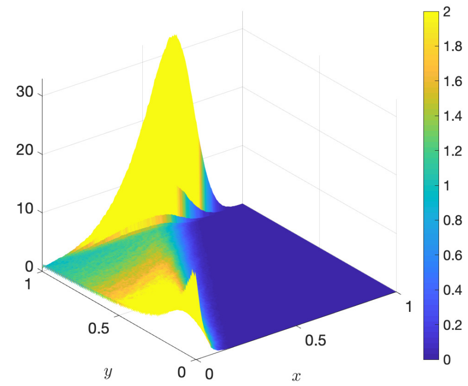


(a) Tip Cells (b) Stalk Cells

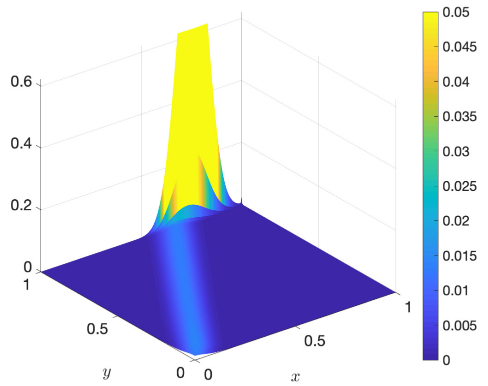
Figure 3: Heat map of (a) tip cell, $n(x, y, t)$, and (b) stalk cell, $e(x, y, t)$ results given by the 2D snail-trail model at $t = 2$, subject to the TAF field $c(x, y) = x$ with $\kappa(x, y) = 2$. The parameter β_e was fitted to the P–ABM results using the numerical methods described in Appendix B ($\beta_e = 4.77$, 95% CI: $[4.73, 4.82]$). The snail-trail model was initialized at $t = 0.2$ using the average P–ABM distribution at that time point.



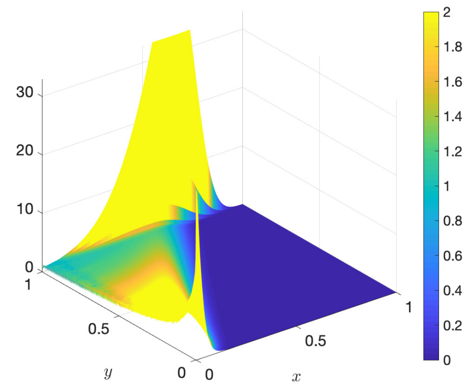
(a) P–ABM, Tip Cell Distribution



(b) P–ABM, Stalk Cell Distribution

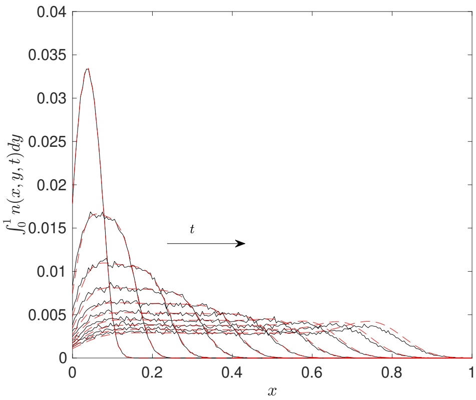


(c) Snail-Trail PDE, Tip Cell Solution

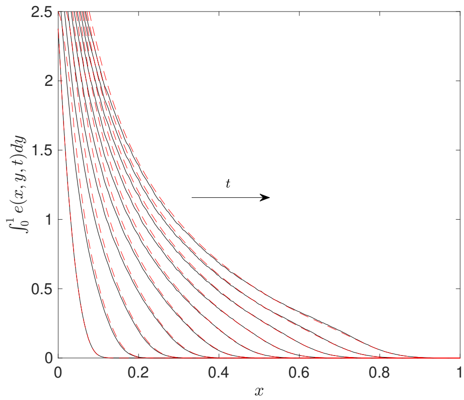


(d) Snail-Trail PDE, Stalk Cell Solution

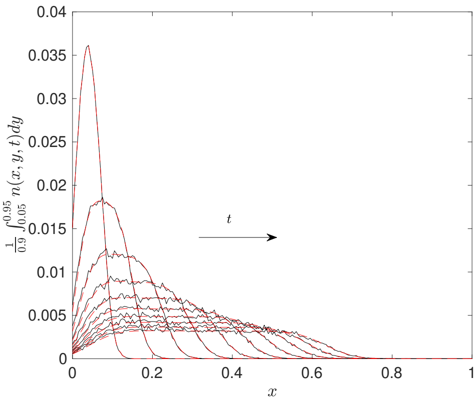
Figure 4: Surface plots of the 2D (a, c) tip cell, $n(x, y, t)$, and (b, d) stalk cell, $e(x, y, t)$ densities given by the (a, b) P–ABM and (c, d) 2D snail-trail model at $t = 2$. Both models are subject to the TAF field $c(x, y) = xy$ and neglect branching and anastomosis events (so that $\lambda = \beta_e = \beta_n = 0$). Note that the snail-trail PDE appears to overestimate the P–ABM stalk cell distribution near $(x, y) = (0, 0)$; this occurs because $\kappa(x, y) \to \infty$ here. The continuous model over estimates the discrete solution near the edge $y = 1$, which is likely due to an edge effect. The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution (see Appendix B of the main text for details). The P–ABM initial condition is described in Appendix A of the main text. For colors, we refer to the online article.



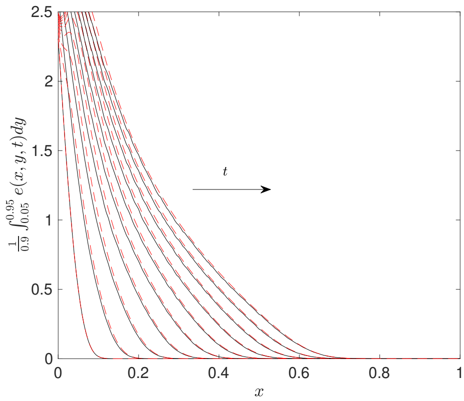
(a) Tip Cells, $y \in (0, 1)$



(b) Stalk Cells, $y \in (0, 1)$

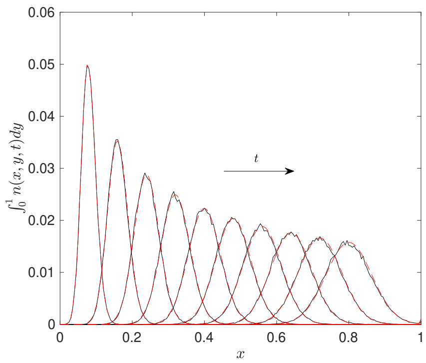


(c) Tip Cells, $y \in (0.05, 0.95)$

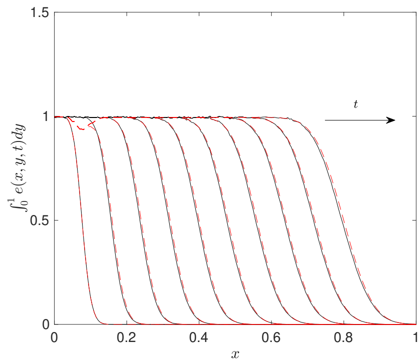


(d) Stalk Cells, $y \in (0.05, 0.95)$

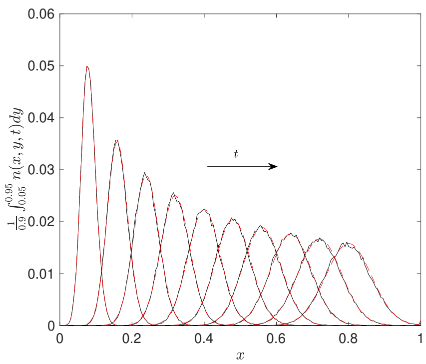
Figure 5: Solutions of the (a, c) tip cell, $n(x, y, t)$, and (b, d) stalk cell, $e(x, y, t)$ densities given by the P–ABM and 2D snail-trail model subject to the TAF field $c(x, y) = xy$, column averaged in the y-direction, at $t = 0.2$, 0.4, ..., 2, with $\lambda = \beta_e = \beta_n = 0$. Column averages were computed over the interval (a, b) $y \in [0, 1]$ and (c, d) $y \in [0.05, 0.95]$, in order to determine if edge effects create differences between the two sets of results. The value of κ was taken to be constant and was computed using a nonlinear least squares fit to the P–ABM data ($\kappa = 3.448$, 95% CI: $[3.445, 3.451]$; see Appendix B of the main text for details on the numerical methods). Key: P–ABM distribution (solid black lines); column averaged 2D snail-trail solution (red dashed lines). The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.



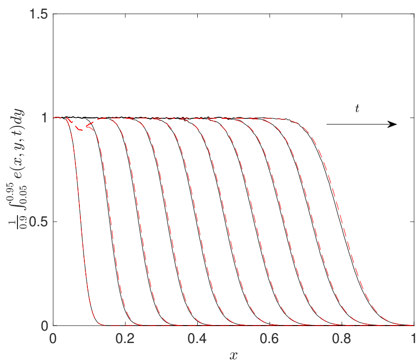
(a) Tip Cells, $y \in (0, 1)$



(b) Stalk Cells, $y \in (0, 1)$

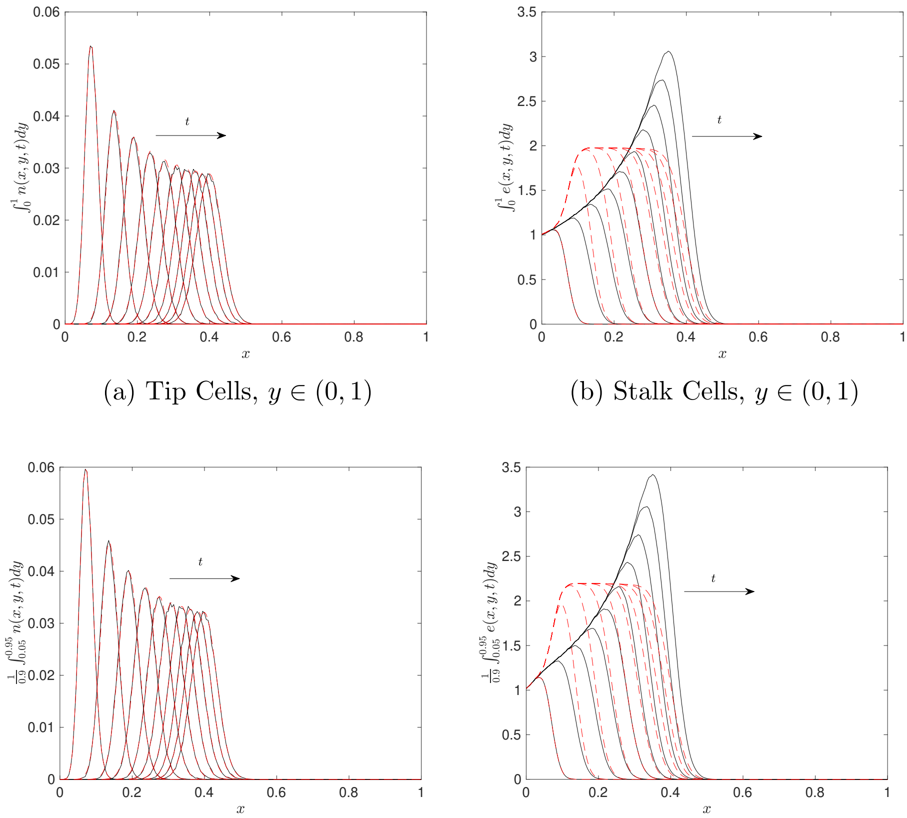


(c) Tip Cells, $y \in (0.05, 0.95)$



(d) Stalk Cells, $y \in (0.05, 0.95)$

Figure 6: Solutions of the (a, c) tip cell, $n(x, y, t)$, and (b, d) stalk cell, $e(x, y, t)$ densities given by the P–ABM and 2D snail-trail model subject to the TAF field $c(x, y) = x$, column averaged in the y-direction, at $t = 0.2$, 0.4, ..., 2, with $\lambda = \beta_e = \beta_n = 0$. Column averages were computed over the interval (a, b) $y \in [0, 1]$ or (c, d) $y \in [0.05, 0.95]$, in order to determine if there were edge effects. The value of κ was taken to be constant and was computed using a nonlinear least squares fit to the P–ABM data ($\kappa = 1.9891$, 95% CI: $[1.9890, 1.9893]$; see Appendix B of the main text for details on the numerical methods). Key: P–ABM distribution (solid black lines); column averaged 2D snail-trail solution (red dashed lines). The computed value of κ is within 1% of the expected value of 2 predicted from equation (14) of the main text. The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.



(a) Tip Cells, $y \in (0, 1)$

(b) Stalk Cells, $y \in (0, 1)$

(c) Tip Cells, $y \in (0.05, 0.95)$

(d) Stalk Cells, $y \in (0.05, 0.95)$

Figure 7: Solutions of the (a, c) tip cell, $n(x, y, t)$, and (b, d) stalk cell, $e(x, y, t)$ densities given by the P–ABM and 2D snail-trail model subject to the TAF field $c(x, y) = 1 - (x - \frac{1}{2})^2 - (y - \frac{1}{2})^2$, column averaged in the y-direction, at $t = 0.2$, 0.4, ..., 2, with $\lambda = \beta_e = \beta_n = 0$. Column averages were computed over the interval (a, b) $y \in [0, 1]$ and (c, d) $y \in [0.05, 0.95]$, in order to determine if edge effects create differences between the two sets of results. The value of κ was taken to be constant and was computed using a nonlinear least squares fit to the P–ABM data ($\kappa = 3.448$, 95% CI: $[3.445, 3.451]$; see Appendix B of the main text for details on the numerical methods). Key: P–ABM distribution (solid black lines); column averaged 2D snail-trail solution (red dashed lines). The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.

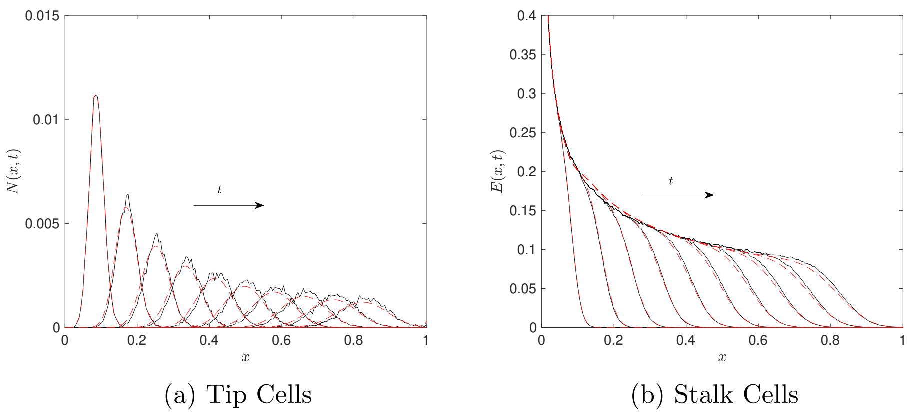
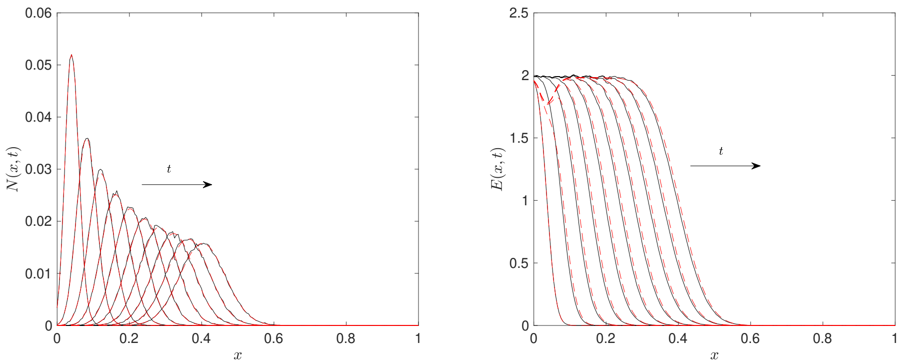
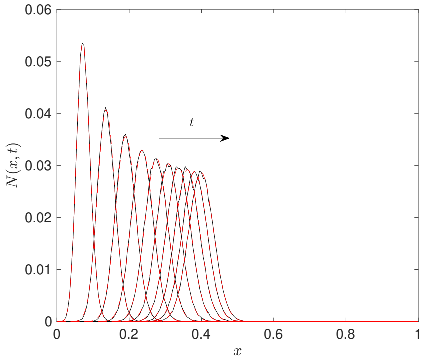


Figure 8: Solutions of the (a) tip cell, $N(x,t)$, and (b) stalk cell, $E(x,t)$ densities given by the P–ABM and 1D snail-trail model at $t = 0.2$, 0.4, ..., 2. The P–ABM results have been column averaged over the interval $y \in [0,1]$, and are subject to the TAF field $c(x,y) = x$. The 1D snail-trail PDE is subject to the column averaged TAF field $C(x) = x$ (so that $\widetilde{\kappa}(x) = 2$), and uses the parameter values listed in Table I of the main text. The value of the parameter β_e was fitted to the column averaged P–ABM data using a nonlinear least squares method ($\beta_e = 4.61$, 95% CI: $[4.58, 4.64]$; see Appendix B of the main text for details on the numerical methods). Key: P–ABM distribution (solid black lines); 1D snail-trail solution (red dashed lines). The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.

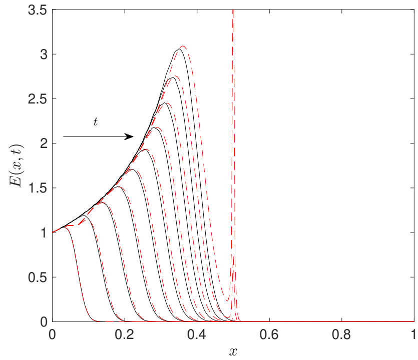


(a) Tip Cells (b) Stalk Cells

Figure 9: Solutions of the (a) tip cell, $N(x,t)$, and (b) stalk cell, $E(x,t)$ densities given by the P–ABM and 1D snail-trail model at $t = 0.2$, 0.4, ..., 2. The P–ABM results have been simulated without branching or anastomosis events, are column averaged over the interval $y \in [0,1]$, and are subject to the TAF field $c(x,y) = 0.5(x+y)$. The 1D snail-trail PDE is subject to the column averaged TAF field $C(x) = 0.5x + 0.25$, with $\lambda = \beta_e = \beta_n = 0$. Key: P–ABM distribution (solid black lines); 1D snail-trail solution (red dashed lines). The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.



(a) Tip Cells



(b) Stalk Cells

Figure 10: Solutions of the (a) tip cell, $N(x,t)$, and (b) stalk cell, $E(x,t)$ densities given by the P–ABM and 1D snail-trail model at $t = 0.2$, 0.4, ..., 2. The P–ABM results have been simulated without branching or anastomosis events, are column averaged over the interval $y \in [0,1]$, and are subject to the TAF field $c(x,y) = 1-(x-0.5)^2-(y-0.5)^2$. The 1D snail-trail PDE is subject to the column averaged TAF field $C(x) = 11/12-(x-1/2)^2$, with $\lambda = \beta_e = \beta_n = 0$. Note the blow-up of the stalk cell solution near $x = 1/2$, which is where the TAF gradient is equal to 0; this occurs because the value of $\widetilde{\kappa}(x) \to \infty$ there. Key: P–ABM distribution (solid black lines); 1D snail-trail solution (red dashed lines). The PDE was simulated on the interval $t \in [0.2, 2]$ and initialized using the average P–ABM distribution at $t = 0.2$ (see Appendix B of the main text for details). For colors, we refer to the online article.